

10/532441

JC20 Rec'd PCT/PTO 22 APR 2005

1cfcc01!.TXT
SEQUENCE LISTING

<110> The Trustees of the University of Pennsylvania
<120> Identification of Antimycobacterial targets and the Inhibition
Thereof as a Treatment for Infectious Diseases
<130> UPFT0001-100
<150> PCT/US03/33524
<151> 2003-10-22
<150> US 60/420,131
<151> 2002-10-22
<160> 12
<170> PatentIn version 3.2
<210> 1
<211> 463
<212> PRT
<213> M. tuberculosis H37Rv
<400> 1

Met Ser Pro Gln Gln Glu Pro Thr Ala Gln Pro Pro Arg Arg His Arg
1 5 10 15

Val Val Ile Ile Gly Ser Gly Phe Gly Gly Leu Asn Ala Ala Lys Lys
20 25 30

Leu Lys Arg Ala Asp Val Asp Ile Lys Leu Ile Ala Arg Thr Thr His
35 40 45

His Leu Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Ile Ser
50 55 60

Glu Gly Glu Ile Ala Pro Pro Thr Arg Val Val Leu Arg Lys Gln Arg
65 70 75 80

Asn Val Gln Val Leu Leu Gly Asn Val Thr His Ile Asp Leu Ala Gly
85 90 95

Gln Cys Val Val Ser Glu Leu Leu Gly His Thr Tyr Gln Thr Pro Tyr
100 105 110

Asp Ser Leu Ile Val Ala Ala Gly Ala Gly Gln Ser Tyr Phe Gly Asn
115 120 125

Asp His Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp Ala
130 135 140

Leu Glu Leu Arg Gly Arg Ile Leu Ser Ala Phe Glu Gln Ala Glu Arg
Page 1

1cfcc01!.TXT

145		150		155		160									
Ser	Ser	Asp	Pro	Glu 165	Arg	Arg	Ala	Lys	Leu 170	Leu	Thr	Phe	Thr	Val 175	Val
Gly	Ala	Gly	Pro 180	Thr	Gly	Val	Glu	Met 185	Ala	Gly	Gln	Ile	Ala	Glu	Leu
Ala	Glu	His 195	Thr	Leu	Lys	Gly	Ala 200	Phe	Arg	His	Ile	Asp 205	Ser	Thr	Lys
Ala	Arg 210	Val	Ile	Leu	Leu	Asp 215	Ala	Ala	Pro	Ala	Val 220	Leu	Pro	Pro	Met
Gly 225	Ala	Lys	Leu	Gly	Gln 230	Arg	Ala	Ala	Ala	Arg 235	Leu	Gln	Lys	Leu	Gly 240
Val	Glu	Ile	Gln	Leu 245	Gly	Ala	Met	Val	Thr 250	Asp	Val	Asp	Arg	Asn 255	Gly
Ile	Thr	Val	Lys 260	Asp	Ser	Asp	Gly	Thr 265	Val	Arg	Arg	Ile	Glu 270	Ser	Ala
Cys	Lys	Val 275	Trp	Ser	Ala	Gly	Val 280	Ser	Ala	Ser	Arg	Leu 285	Gly	Arg	Asp
Leu	Ala 290	Glu	Gln	Ser	Arg	Val 295	Glu	Leu	Asp	Arg	Ala 300	Gly	Arg	Val	Gln
Val 305	Leu	Pro	Asp	Leu	Ser 310	Ile	Pro	Gly	Tyr	Pro 315	Asn	Val	Phe	Val	Val 320
Gly	Asp	Met	Ala	Ala 325	Val	Glu	Gly	Val	Pro 330	Gly	Val	Ala	Gln	Gly 335	Ala
Ile	Gln	Gly	Ala 340	Lys	Tyr	Val	Ala	Ser 345	Thr	Ile	Lys	Ala	Glu 350	Leu	Ala
Gly	Ala	Asn 355	Pro	Ala	Glu	Arg	Glu 360	Pro	Phe	Gln	Tyr	Phe 365	Asp	Lys	Gly
Ser	Met 370	Ala	Thr	Val	Ser	Arg 375	Phe	Ser	Ala	Val	Ala 380	Lys	Ile	Gly	Pro
Val 385	Glu	Phe	Ser	Gly	Phe 390	Ile	Ala	Trp	Leu	Ile 395	Trp	Leu	Val	Leu	His 400

1cfcc01!.TXT

Leu Ala Tyr Leu Ile Gly Phe Lys Thr Lys Ile Thr Thr Leu Leu Ser
405 410 415

Trp Thr Val Thr Phe Leu Ser Thr Arg Arg Gly Gln Leu Thr Ile Thr
420 425 430

Asp Gln Gln Ala Phe Ala Arg Thr Arg Leu Glu Gln Leu Ala Glu Leu
435 440 445

Ala Ala Glu Ala Gln Gly Ser Ala Ala Ser Ala Lys Val Ala Ser
450 455 460

<210> 2
<211> 1392
<212> DNA
<213> M. tuberculosis H37Rv

<400> 2
atgagtcctccc agcaagaacc cacagcgcaa ccacctcgta ggcatacgagt tgtgatcatc 60
ggatctgggt tcggcgggct aaacgcggca aagaagctca agcggggccga cgttgacatc 120
aagctgatcg cgcgcaccac ccatcacctg ttccagccgc tgctgtacca agtggccacc 180
gggattatct ccgagggaga aatcgctccg ccgacccggg tcgtgctgcg taagcagcgc 240
aatgtccagg tactgttggg caacgtcacc cacatcgacc tggccgggca gtgcgtcgtc 300
tcggaattgc tcggtcacac ctaccaaacc ccctacgaca gcctgatcgt cgccgcgggt 360
gctggccagt cttatttcgg caacgaccat ttcgccgaat tcgcacccgg catgaagtcc 420
atcgacgacg cgttggagtt gcgtggccgc atattgagcg ctttcgagca agccgaacgg 480
tccagcgatc cggaacggcg ggccaagcta ctgacattca ccgttgctcg ggctggcccc 540
accggtgttg aaatggccgg acagatcgcc gagctggccg agcacacgtt gaagggcgca 600
ttccggcaca tcgactcgac caaggcgcggtg tgattctgc ttgacgccgc cccggcggtg 660
ctgccaccga tgggcgcaaa gctcggtcag cgggcggctg cccggttgca gaagctgggc 720
gtggaaatcc agctgggtgc gatggtcacc gacgtcgacc gcaacggcat caccgtcaag 780
gactccgacg gcaccgtccg gcgcatcgag tcggcctgca aggtctggtc ggccggggtt 840
tcggccagtc ggttgggcag ggaccttgcc gagcaatcac gggttgagct cgaccgggcc 900
ggccgggtcc aagtgtgtcc cgacctgtcc attcccgggt acccgaacgt gttcgtggtg 960
ggcgatatgg ccgctgtgga ggggtgtgcc ggtgtggcgc agggcgccat ccagggggcg 1020
aaatacgtcg ccagcacgat caaggccgaa ctggccggcg ccaacccggc ggagcgtgag 1080
ccattccagt acttcgaaa gggatcgatg gccacggttt cgagggtttc ggcggtggcc 1140
aagatcggtc ccgttgagtt cagcggcttt atcgccctggc tgatttggtt ggtgctgcac 1200
ctggcgtacc tgatcgggtt caagaccaag atcaccactc tgctgtcgtg gacggtgact 1260

1cfcc01!.TXT

ttcctcagta ctcgccgcgg ccagctgacc atcaccgacc agcaggcatt tgcgcgaacg 1320
cggctcgaac agctggccga gctggccgcc gaggcgcagg gctcagcggc aagcgctaag 1380
gtggccagct ag 1392

<210> 3
<211> 470
<212> PRT
<213> M. tuberculosis H37Rv
<400> 3

Met Thr Leu Ser Ser Gly Glu Pro Ser Ala Val Gly Gly Arg His Arg
1 5 10 15
Val Val Ile Ile Gly Ser Gly Phe Gly Gly Leu Asn Ala Ala Lys Ala
20 25 30
Leu Lys Arg Ala Asp Val Asp Ile Thr Leu Ile Ser Lys Thr Thr Thr
35 40 45
His Leu Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu Ser
50 55 60
Glu Gly Asp Ile Ala Pro Thr Thr Arg Leu Ile Leu Arg Arg Gln Lys
65 70 75 80
Asn Val Arg Val Leu Leu Gly Glu Val Asn Ala Ile Asp Leu Lys Ala
85 90 95
Gln Thr Val Thr Ser Lys Leu Met Asp Met Thr Thr Val Thr Pro Tyr
100 105 110
Asp Ser Leu Ile Val Ala Ala Gly Ala Gln Gln Ser Tyr Phe Gly Asn
115 120 125
Asp Glu Phe Ala Thr Phe Ala Pro Gly Met Lys Thr Ile Asp Asp Ala
130 135 140
Leu Glu Leu Arg Gly Arg Ile Leu Gly Ala Phe Glu Ala Ala Glu Val
145 150 155 160
Ser Thr Asp His Ala Glu Arg Glu Arg Arg Leu Thr Phe Val Val Val
165 170 175
Gly Ala Gly Pro Thr Gly Val Glu Val Ala Gly Gln Ile Val Glu Leu
180 185 190

1cfcc01!.TXT

Ala Glu Arg Thr Leu Ala Gly Ala Phe Arg Thr Ile Thr Pro Ser Glu
 195 200 205
 Cys Arg Val Ile Leu Leu Asp Ala Ala Pro Ala Val Leu Pro Pro Met
 210 215 220
 Gly Pro Lys Leu Gly Leu Lys Ala Gln Arg Arg Leu Glu Lys Met Asp
 225 230 235 240
 Val Glu Val Gln Leu Asn Ala Met Val Thr Ala Val Asp Tyr Lys Gly
 245 250 255
 Ile Thr Ile Lys Glu Lys Asp Gly Gly Glu Arg Arg Ile Glu Cys Ala
 260 265 270
 Cys Lys Val Trp Ala Ala Gly Val Ala Ala Ser Pro Leu Gly Lys Met
 275 280 285
 Ile Ala Glu Gly Ser Asp Gly Thr Glu Ile Asp Arg Ala Gly Arg Val
 290 295 300
 Ile Val Glu Pro Asp Leu Thr Val Lys Gly His Pro Asn Val Phe Val
 305 310 315 320
 Val Gly Asp Leu Met Phe Val Pro Gly Val Pro Gly Val Ala Gln Gly
 325 330 335
 Ala Ile Gln Gly Ala Arg Tyr Ala Thr Thr Val Ile Lys His Met Val
 340 345 350
 Lys Gly Asn Asp Asp Pro Ala Asn Arg Lys Pro Phe His Tyr Phe Asn
 355 360 365
 Lys Gly Ser Met Ala Thr Ile Ser Arg His Ser Ala Val Ala Gln Val
 370 375 380
 Gly Lys Leu Glu Phe Ala Gly Tyr Phe Ala Trp Leu Ala Trp Leu Val
 385 390 395 400
 Leu His Leu Val Tyr Leu Val Gly Tyr Arg Asn Arg Ile Ala Ala Leu
 405 410 415
 Phe Ala Trp Gly Ile Ser Phe Met Gly Arg Ala Arg Gly Gln Met Ala
 420 425 430
 Ile Thr Ser Gln Met Ile Tyr Ala Arg Leu Val Met Thr Leu Met Glu
 435 440 445

1cfcc01!.TXT

Gln Gln Ala Gln Gly Ala Leu Ala Ala Ala Glu Gln Ala Glu His Ala
450 455 460

Glu Gln Glu Ala Ala Gly
465 470

<210> 4
<211> 1413
<212> DNA
<213> M. tuberculosis H37Rv

```
<400> 4
atgacgctct catctggtga accctcggcc gtcggcgggc gccatcgcgt ggatcatcatc 60
ggtagtggat tcggcggcct gaatgcggcc aaggcgctta aacgggcgga tgtcgacatc 120
acgctgatct ccaagacaac gaccacctg ttccagccgc tgctgtatca agtggccacc 180
gggatcttgt ccgagggcga cattgccccg accacccggc tgatcctgcg ccggcaaaaag 240
aacgtccggg tgttgctggg cgaggtcaac gcgatcgacc tgaaagcgca gacggtcacg 300
tcgaaattga tggacatgac cacggtgacg ccgtacgaca gcctcatcgt ggccgccggc 360
gcacagcagt cctacttcgg caacgacgaa ttcgccacct tcgcgcccgg aatgaagacc 420
atcgacgacg cgctggagct gcgcggccgc atcctgggcg cgttcgaggc cgccgaggtc 480
agcaccgacc atgccgaacg ggagcggcgc ctgacgttcg tcgtcgtcgg cgctgggccg 540
accggcgctc aggtggctgg gcagatcgtc gagctcgccg agcgcaccct ggcaggcgcg 600
tttaggacca tcacgcccag tgagtgccgg gtgatcctgc tcgacgccgc acccgcggtg 660
ttgccgccga tgggtccaaa gctgggtctc aaggcacaac ggcggtgga aaagatggac 720
gtcgagggtc aactcaacgc gatggtgacc gcggtcgact acaaaggcat caccatcaag 780
gaaaaggacg gcggcgaacg ccgcatcgaa tgcgcgtgca aggtttgggc ggccggcggtg 840
gcggccagcc cgctgggcaa gatgatcgcc gagggatccg acggaaccga aatcgaccgg 900
gccggaaggg tgatcgtgga acccgatctc accgtcaagg gacatccgaa cgtcttcgta 960
gtcggcgatc tgatgttcgt gcccggcgta cccgggggtg ctcagggcgc gatccagggg 1020
gcccgatagc ccaccacggt gatcaaacac atggtcaagg gcaatgacga cccagccaat 1080
cgcaagccgt tccattactt caacaagggc agcatggcga cgatctcccg ccacagcgcc 1140
gtcgcgcagg tcggcaagct ggagtttgcc ggggtacttcg cctggctggc gtggctggtg 1200
ctgcacctgg tctacctggg cggctatcgg aaccgcatcg cagccctggt cgccctggggg 1260
atctccttca tgggccgcgc ccgcggccag atggccatca ccagccagat gatctacgcc 1320
aggttagtga tgaccttgat ggaacagcag gcacaaggag cgctggcagc cgccgaacag 1380
gccgagcacg ccgagcaaga ggcagcgggt tag 1413
```

1cfcc01!.TXT

<210> 5
 <211> 219
 <212> PRT
 <213> M. tuberculosis CDC1551

<400> 5

Met Phe Asp Gly Val Ala Arg Lys Tyr Asp Leu Thr Asn Thr Val Leu
 1 5 10 15

Ser Leu Gly Gln Asp Arg Tyr Trp Arg Arg Ala Thr Arg Ser Ala Leu
 20 25 30

Arg Ile Gly Pro Gly Gln Lys Val Leu Asp Leu Ala Ala Gly Thr Ala
 35 40 45

Val Ser Thr Val Glu Leu Thr Lys Ser Gly Ala Trp Cys Val Ala Ala
 50 55 60

Asp Phe Ser Val Gly Met Leu Ala Ala Gly Ala Ala Arg Lys Val Pro
 65 70 75 80

Lys Val Ala Gly Asp Ala Thr Arg Leu Pro Phe Gly Asp Asp Val Phe
 85 90 95

Asp Ala Val Thr Ile Ser Phe Gly Leu Arg Asn Val Ala Asn Gln Gln
 100 105 110

Ala Ala Leu Arg Glu Met Ala Arg Val Thr Arg Pro Gly Gly Arg Leu
 115 120 125

Leu Val Cys Glu Phe Ser Thr Pro Thr Asn Ala Leu Phe Ala Thr Ala
 130 135 140

Tyr Lys Glu Tyr Leu Met Arg Ala Leu Pro Arg Val Ala Arg Ala Val
 145 150 155 160

Ser Ser Asn Pro Glu Ala Tyr Glu Tyr Leu Ala Glu Ser Ile Arg Ala
 165 170 175

Trp Pro Asp Gln Ala Val Leu Ala His Gln Ile Ser Arg Ala Gly Trp
 180 185 190

Ser Gly Val Arg Trp Arg Asn Leu Thr Gly Gly Ile Val Ala Leu His
 195 200 205

Ala Gly Tyr Lys Pro Gly Lys Gln Thr Pro Gln
 210 215

1cfcc01!.TXT

<210> 6
 <211> 660
 <212> DNA
 <213> M. tuberculosis CDC1551

<400> 6
 atgttcgatg gcgtcgcccg caagtatgac ctgaccaata ccgtgttgct cctgggccag 60
 gaccgggtatt ggcggcgagc cactcggctg gcgctgcgga tcgggcccgg ccaaaaggct 120
 ctggacctgg ccgcgggcac cgccgtgtcc accgtagagc tcaccaaatac gggcgctgg 180
 tgtgtggctg ccgatttttc ggtcggcatg cttgcggcgg gcgctgcgcg caagggtccc 240
 aaggctgccg gtgacgccac ccggctgccg tttggtgacg acgtgttcga tgcggtcacc 300
 atcagtttcg ggctgcgtaa cgctgcgaaac cagcaagcgg cgctgcggga aatggctcgt 360
 gtcacccggc cgggcgggag gctactagtg tgcgaattct ccacgccac caatgcgttg 420
 ttcgccaccg cctacaagga atacttgatg cgggcgctgc cccgggtggc gcgggcggtg 480
 tctagcaacc ccgaggccta cgagtacctc gcggagtcga tcagggcctg gcccgaccag 540
 gcggtgctgg cgcaccagat ttcgcgggcc ggggtggtcgg ggggtgcggtg gcgcaacctg 600
 accggcggca tcgtagctct gcatgccgga tacaaccccg gcaaacaac cccgcagtga 660

<210> 7
 <211> 486
 <212> PRT
 <213> M. tuberculosis CDC1551

<400> 7

Met	Ser	Val	Thr	Pro	Asn	Ala	Gly	Cys	Val	Asp	Val	Val	Ile	Val	Gly
1				5				10						15	
Ala	Gly	Ile	Ser	Gly	Leu	Gly	Ala	Ala	Tyr	Arg	Ile	Ile	Glu	Arg	Asn
			20				25						30		
Pro	Gln	Leu	Thr	Tyr	Thr	Ile	Leu	Glu	Arg	Arg	Ala	Arg	Ile	Gly	Gly
		35				40					45				
Thr	Trp	Asp	Leu	Phe	Arg	Tyr	Pro	Gly	Val	Arg	Ser	Asp	Ser	Ser	Ile
	50					55					60				
Phe	Thr	Leu	Pro	Phe	Pro	Tyr	Glu	Pro	Trp	Thr	Arg	Glu	Glu	Gly	Ile
65				70					75					80	
Ala	Asp	Gly	Ala	His	Ile	Arg	Glu	Tyr	Leu	Thr	Asp	Met	Ala	His	Lys
			85					90					95		
Tyr	Gly	Ile	Asp	Arg	His	Ile	Glu	Phe	Asn	Ser	Tyr	Val	Arg	Ala	Ala
			100					105					110		

1cfcc01!.TXT

Asp Trp Asp Ser Ser Thr Asp Thr Trp Thr Val Thr Phe Glu Gln Asn
115 120 125

Gly Val His Lys His Tyr Arg Ser Arg Phe Val Phe Phe Gly Ser Gly
130 135 140

Tyr Tyr Asn Tyr Asp Glu Gly Tyr Thr Pro Asp Phe Gly Gly Ile Glu
145 150 155 160

Lys Phe Gly Gly Ala Val Val His Pro Gln His Trp Pro Glu Asp Leu
165 170 175

Asp Tyr Thr Gly Lys Lys Ile Val Val Ile Gly Ser Gly Ala Thr Ala
180 185 190

Val Thr Leu Ile Pro Ser Leu Thr Asp Arg Ala Glu Lys Val Thr Met
195 200 205

Leu Gln Arg Ser Pro Thr Tyr Leu Ile Ser Ala Ser Lys Tyr Ser Thr
210 215 220

Phe Ala Ala Val Val Arg Lys Ala Leu Pro Pro Lys Thr Ser His Leu
225 230 235 240

Ile Val Arg Met Tyr Asn Ala Leu Leu Glu Ala Val Phe Trp Phe Leu
245 250 255

Ser Arg Lys Thr Pro Val Phe Val Lys Trp Leu Leu Arg Arg Thr Ala
260 265 270

Ile Lys Asn Leu Pro Glu Gly Tyr Asp Ile Glu Thr His Phe Thr Pro
275 280 285

Arg Tyr Asn Pro Trp Asp Gln Arg Leu Cys Leu Ile Pro Asp Ala Asp
290 295 300

Leu Tyr Asn Ala Ile Thr Ser Gly Arg Ala Glu Val Val Thr Asp His
305 310 315 320

Ile Asp His Phe Asp Ala Thr Gly Ile Ala Leu Lys Ser Gly Gly His
325 330 335

Leu Asp Ala Asp Ile Ile Val Thr Ala Thr Gly Leu Gln Leu Gln Ala
340 345 350

Leu Gly Gly Ala Ala Ile Ser Leu Asp Gly Val Glu Ile Asp Pro Arg

355

360

365

Asp Arg Phe Val Tyr Lys Ala His Met Leu Glu Asp Val Pro Asn Leu
 370 375 380

Phe Trp Cys Val Gly Tyr Thr Asn Ala Ser Trp Thr Leu Arg Ala Asp
 385 390 395 400

Met Thr Ala Arg Ala Thr Ala Lys Leu Leu Ala His Met Ala Ala His
 405 410 415

Gly His Thr Arg Ala Ala Pro His Leu Gly Asp Glu Pro Met Asp Glu
 420 425 430

Lys Pro Ser Trp Asp Ile Gln Ala Gly Tyr Val Lys Arg Ala Pro Tyr
 435 440 445

Ala Leu Pro Lys Ser Gly Thr Lys Arg Pro Trp Asn Val Arg Gln Asn
 450 455 460

Tyr Leu Ala Asp Ala Ile Asp Tyr Arg Phe Asp Arg Ile Glu Glu Ala
 465 470 475 480

Met Val Phe Gly Ala Ala
 485

<210> 8
 <211> 1461
 <212> DNA
 <213> M. tuberculosis CDC1551

<400> 8
 tcatgccgcg ccgaacacca ttgcctcctc gatgcggtcg aatcggtagt cgatggcgtc 60
 ggccaagtag ttctgtcgta cattccacgg ccgcttggtg ccggacttgg gcagcgcgta 120
 cggcgcccgc ttcacatagc cggcctgaat gtcccaggac ggtttctcgt ccatcggtc 180
 gtcgcccagg tgcggggcgg cgcgcgtgtg tccatgggcg gccatgtgtg ccagtagttt 240
 tgccgtcgcc cgggccgtca tgtcggcgcg cagcgtccag gacgcgttcg tgtaaccac 300
 acaccagaac aggttgggca cgtcttcgag catgtgcgcc ttgtagacaa agcgatccc 360
 agggtcgatc tcgacgccgt cgaggctgat cgcgggcccg ccaagcgctt gcaactgcag 420
 gccggtggcg gtgacgataa tgtccgcata gaggtgcca ccggatttga gtgcaatacc 480
 ggtggcgtcg aagtggtcga tatggtcggt gaccacctcg gcgcggccgc tggatgatggc 540
 gttgtacagg tcggcgtccg ggatcaggca cagtcgctga tcccacgggt tgtaccgcgg 600
 cgtgaagtgg gtttcgatgt cgtagccctc gggcagattt ttgatcgcgg tacggcgtag 660

1cfcc01!.TXT

cagccatttc acgaacaccg gtgtcttgcg ggacaagaac cagaacaccg cttccaataa 720
cgcgttgtac attcggacaa tcaagtgaga agttttggga ggcaacgctt tacgaacaac 780
ggcggcgaac gtgctgtatt tggatgccga gatcaggtag gtcggggatc gctgcagcat 840
ggttaccttt tcggcccgggt cggtcagcga ggggatcagt gtgaccgcgg tggccccgct 900
gccgatcacc acgatcttct tgccgggtga gtccagatcc tctggccagt gctggggatg 960
cactaccgcg ccgccaaact tctcgatgcc tccgaagtcg ggggtgtagc cctcgtcata 1020
gttgtagtag ccgctgccga agaacacgaa ccggctgcgg tagtgcttgt gcacgccgtt 1080
ctgctcgaag gtgacgggcc aggtatcggg ggatgagtc cagtccgctg cgcgaacgta 1140
gctgttgaac tcgatgtggc gatcgatgcc gtacttgctg gccatgtcgg tgaggtactc 1200
gcggatgtgg gcgccgtcgg cgatgccttc ttcgcgggtc cacggctcgt agggaaacgg 1260
cagcgtgaag atgctgctgt cggagcgcac gccggggtag cggaacagat cccaggtgcc 1320
gccgatccgc gcacgccttt ccaggatggg gtaggtcagc tgcgggttgc gttcgatgat 1380
ccggtaggcc gcgcccagtc cggagatgcc ggcgccgacg atgacgacgt cgacacagcc 1440
ggcgtttgga gtcacgctca t 1461

<210> 9
<211> 583
<212> PRT
<213> M. tuberculosis H37Rv

<400> 9

Met Thr Ala Gln His Asn Ile Val Val Ile Gly Gly Gly Gly Ala Gly
1 5 10 15

Leu Arg Ala Ala Ile Ala Ile Ala Glu Thr Asn Pro His Leu Asp Val
20 25 30

Ala Ile Val Ser Lys Val Tyr Pro Met Arg Ser His Thr Val Ser Ala
35 40 45

Glu Gly Gly Ala Ala Ala Val Thr Gly Asp Asp Asp Ser Leu Asp Glu
50 55 60

His Ala His Asp Thr Val Ser Gly Gly Asp Trp Leu Cys Asp Gln Asp
65 70 75 80

Ala Val Glu Ala Phe Val Ala Glu Ala Pro Lys Glu Leu Val Gln Leu
85 90 95

Glu His Trp Gly Cys Pro Trp Ser Arg Lys Pro Asp Gly Arg Val Ala
100 105 110

1cfcc01!.TXT

Val Arg Pro Phe Gly Gly Met Lys Lys Leu Arg Thr Trp Phe Ala Ala
115 120 125

Asp Lys Thr Gly Phe His Leu Leu His Thr Leu Phe Gln Arg Leu Leu
130 135 140

Thr Tyr Ser Asp Val Met Arg Tyr Asp Glu Trp Phe Ala Thr Thr Leu
145 150 155 160

Leu Val Asp Asp Gly Arg Val Cys Gly Leu Val Ala Ile Glu Leu Ala
165 170 175

Thr Gly Arg Ile Glu Thr Ile Leu Ala Asp Ala Val Ile Leu Cys Thr
180 185 190

Gly Gly Cys Gly Arg Val Phe Pro Phe Thr Thr Asn Ala Asn Ile Lys
195 200 205

Thr Gly Asp Gly Met Ala Leu Ala Phe Arg Ala Gly Ala Pro Leu Lys
210 215 220

Asp Met Glu Phe Val Gln Tyr His Pro Thr Gly Leu Pro Phe Thr Gly
225 230 235 240

Ile Leu Ile Thr Glu Ala Ala Arg Ala Glu Gly Gly Trp Leu Leu Asn
245 250 255

Lys Asp Gly Tyr Arg Tyr Leu Gln Asp Tyr Asp Leu Gly Lys Pro Thr
260 265 270

Pro Glu Pro Arg Leu Arg Ser Met Glu Leu Gly Pro Arg Asp Arg Leu
275 280 285

Ser Gln Ala Phe Val His Glu His Asn Lys Gly Arg Thr Val Asp Thr
290 295 300

Pro Tyr Gly Pro Val Val Tyr Leu Asp Leu Arg His Leu Gly Ala Asp
305 310 315 320

Leu Ile Asp Ala Lys Leu Pro Phe Val Arg Glu Leu Cys Arg Asp Tyr
325 330 335

Gln His Ile Asp Pro Val Val Glu Leu Val Pro Val Arg Pro Val Val
340 345 350

His Tyr Met Met Gly Gly Val His Thr Asp Ile Asn Gly Ala Thr Thr
355 360 365

1cfcc01!.TXT

Leu Pro Gly Leu Tyr Ala Ala Gly Glu Thr Ala Cys Val Ser Ile Asn
 370 375 380
 Gly Ala Asn Arg Leu Gly Ser Asn Ser Leu Pro Glu Leu Leu Val Phe
 385 390 395 400
 Gly Ala Arg Ala Gly Arg Ala Ala Ala Asp Tyr Ala Ala Arg His Gln
 405 410 415
 Lys Ser Asp Arg Gly Pro Ser Ser Ala Val Arg Ala Gln Ala Arg Thr
 420 425 430
 Glu Ala Leu Arg Leu Glu Arg Glu Leu Ser Arg His Gly Gln Gly Gly
 435 440 445
 Glu Arg Ile Ala Asp Ile Arg Ala Asp Met Gln Ala Thr Leu Glu Ser
 450 455 460
 Ala Ala Gly Ile Tyr Arg Asp Gly Pro Thr Leu Thr Lys Ala Val Glu
 465 470 475 480
 Glu Ile Arg Val Leu Gln Glu Arg Phe Ala Thr Ala Gly Ile Asp Asp
 485 490 495
 His Ser Arg Thr Phe Asn Thr Glu Leu Thr Ala Leu Leu Glu Leu Ser
 500 505 510
 Gly Met Leu Asp Val Ala Leu Ala Ile Val Glu Ser Gly Leu Arg Arg
 515 520 525
 Glu Glu Ser Arg Gly Ala His Gln Arg Thr Asp Phe Pro Asn Arg Asp
 530 535 540
 Asp Glu His Phe Leu Ala His Thr Leu Val His Arg Glu Ser Asp Gly
 545 550 555 560
 Thr Leu Arg Val Gly Tyr Leu Pro Val Thr Ile Thr Arg Trp Pro Pro
 565 570 575
 Gly Glu Arg Val Tyr Gly Arg
 580

<210> 10
 <211> 1752
 <212> DNA
 <213> M. tuberculosis H37Rv

1cfcc01!.TXT

<400> 10
 atgaccgccc aacacaacat cgtggttatc ggcggcggtg gtgcgggtct gcgcgccgcg 60
 attgcgatat ccgaaaccaa tccgcacctg gatgtggcga tcgtttccaa ggtgtacccg 120
 atgcgcagcc acaccgtctc ggctgagggc ggcgccgcgg cggtgaccgg tgacgacgac 180
 agcctcgatg aacacgcgca cgacacggta tccggtggcg actggctgtg tgaccaagat 240
 gcggtcgagg ctttcgtggc cgaggcgccc aaagagttgg tgcagctcga gcattggggc 300
 tgtccgtgga gccgtaaacc agacgggcgc gttgccgttc gcccgttcgg cgggatgaag 360
 aagctgcgca cctggtttgc cgccgacaag acgggatttc acctcctgca cacgttgttt 420
 caacggctgc tcacctattc cgacgtcatg cgctatgacg agtggttcgc tacgacgtg 480
 ctggtcgacg acggcagggg atgtggtctg gtcgctatcg agttggcgac cgggcgcac 540
 gagacgatcc ttgccgacgc ggtgattctg tgcaccggcg gatgcgggcg ggtatttcca 600
 ttcaccacca acgcgaacat caagaccggc gacggcatgg cgctcgcatt ccgcgcgggc 660
 gcgcccctaa aagacatgga attcgtccaa taccaccca ccggactgcc gttcaccggg 720
 atcttgatca ccgaggccgc acgagctgaa ggcggctggc tgctcaaaa agacggctac 780
 cgctacctcc aggattacga cctcggcaag cccacgcccg agcccaggct gcgcagtatg 840
 gagctcgggc ccagggaccg actgtcgcag gccttcgtac acgagcacia caaaggaagg 900
 acggtcgaca ccccgtacgg ccccgctgc tcttagacc tgcggcacct gggggcggac 960
 ctgatcgatg caaagttgcc gttcgtacgt gagctgtgcc gcgactacca gcacatcgac 1020
 cccgtggtcg aattgggtccc ggtacgaccg gtagtgact acatgatggg tggcgttcac 1080
 accgatata acggcgccac aacgcttccc gggctatatg ccgcaggtga aacagcctgc 1140
 gtgagcatta atggcgccaa ccgcctgggg tcgaactcgc tgcccagact gctggtgttc 1200
 ggggctcgag cgggccgtgc cgccgcggat tacgcagcgc gccacaaaaa gtcggaccgt 1260
 ggcccgtcgt cggcagtgcg ggctcaggcc cgcaccgagg ctctacggct agagcgtgag 1320
 ctgagccgcc atggccaggg aggcgaacga atcgcgata ttcgggcgga catgcaggcc 1380
 accttgga aa gcgcgcggg tatttatcgt gacggacca ccctcacaa agcggctgag 1440
 gagattcggg tgctgcagga acgattcgcc acggcgggca tcgacgatca cagccgcaca 1500
 ttcaacaccg agctgactgc gctgctcgag ttgtcgggga tgctcgacgt tgcactggcg 1560
 atcgtcgaat cgggttttgc ccgagaagaa tcccgtggcg cacaccagcg aaccgacttt 1620
 ccgaaccggg acgacgagca tttcttggcg cacaccttgg ttcatagaga aagcgacgga 1680
 acgctgcggg tcggctacct tccggtcact atcactcgct ggccaccggg cgaacgcgtg 1740
 tatgggaggt aa 1752

<210> 11

1cfcc01!.TXT

<211> 1232

<212> PRT

<213> M. tuberculosis H37Rv

<400> 11

Met Thr Val Thr Pro His Val Gly Gly Pro Leu Glu Glu Leu Leu Glu
1 5 10 15

Arg Ser Gly Arg Phe Phe Thr Pro Gly Glu Phe Ser Ala Asp Leu Arg
20 25 30

Thr Val Thr Arg Arg Gly Gly Arg Glu Gly Asp Val Phe Tyr Arg Asp
35 40 45

Arg Trp Ser His Asp Lys Val Val Arg Ser Thr His Gly Val Asn Cys
50 55 60

Thr Gly Ser Cys Ser Trp Lys Ile Tyr Val Lys Asp Gly Ile Ile Thr
65 70 75 80

Trp Glu Thr Gln Gln Thr Asp Tyr Pro Ser Val Gly Pro Asp Arg Pro
85 90 95

Glu Tyr Glu Pro Arg Gly Cys Pro Arg Gly Ala Ser Phe Ser Trp Tyr
100 105 110

Ser Tyr Ser Pro Thr Arg Val Arg Tyr Pro Tyr Ala Arg Gly Val Leu
115 120 125

Val Glu Met Tyr Arg Glu Ala Lys Thr Arg Leu Gly Asp Pro Val Leu
130 135 140

Ala Trp Ala Asp Ile Gln Ala Asp Pro Glu Arg Arg Arg Arg Tyr Gln
145 150 155 160

Gln Ala Arg Gly Lys Gly Gly Leu Val Arg Val Ser Trp Ala Glu Ala
165 170 175

Ser Glu Met Val Ala Ala Ala His Val His Thr Ile Lys Thr Tyr Gly
180 185 190

Pro Asp Arg Val Ala Gly Phe Ser Pro Ile Pro Ala Met Ser Met Val
195 200 205

Ser His Ala Ala Gly Ser Arg Phe Val Glu Leu Ile Gly Gly Val Met
210 215 220

Thr Ser Phe Tyr Asp Trp Tyr Ala Asp Leu Pro Val Ala Ser Pro Gln
Page 15

1cfcc01!.TXT

225 230 235 240

val phe Gly Asp Gln Thr Asp val Pro Glu Ser Gly Asp Trp Trp Asp
 245 250 255

Ala Ser Tyr Leu val Met Trp Gly Ser Asn val Pro Ile Thr Arg Thr
 260 265 270

Pro Asp Ala His Trp Met Ala Glu Ala Arg Tyr Arg Gly Ala Lys val
 275 280 285

val val val Ser Pro Asp Tyr Ala Asp Asn Thr Lys Phe Ala Asp Glu
 290 295 300

Trp val Arg Cys Ala Ala Gly Thr Asp Thr Ala Leu Ala Met Ala Met
305 310 315 320

Gly His val Ile Leu Ser Glu Cys Tyr val Arg Asn Gln val Pro Phe
 325 330 335

Phe val Asp Tyr val Arg Arg Tyr Thr Asp Leu Pro Phe Leu Ile Lys
 340 345 350

Leu Glu Lys Arg Gly Asp Leu Leu val Pro Gly Lys Phe Leu Thr Ala
 355 360 365

Ala Asp Ile Gly Glu Glu Ser Glu Asn Ala Ala Phe Lys Pro Ala Leu
370 375 380

Leu Asp Glu Leu Thr Asn Thr val val val Pro Gln Gly Ser Leu Gly
385 390 395 400

Phe Arg Phe Gly Glu Asp Gly val Gly Lys Trp Asn Leu Asp Leu Gly
 405 410 415

Ser val val Pro Ala Leu Ser val Glu Met Asp Lys Ala val Asn Gly
 420 425 430

Asp Arg Ser Ala Glu Leu val Thr Leu Pro Ser Phe Asp Thr Ile Asp
 435 440 445

Gly His Gly Glu Thr val Ser Arg Gly val Pro val Arg Arg Ala Gly
450 455 460

Lys His Leu val Cys Thr val Phe Asp Leu Met Leu Ala His Tyr Gly
465 470 475 480

1cfcc01!.TXT

Val Ala Arg Ala Gly Leu Pro Gly Glu Trp Pro Thr Gly Tyr His Asp
485 490 495

Arg Thr Gln Gln Asn Thr Pro Ala Trp Gln Glu Ser Ile Thr Gly Val
500 505 510

Pro Ala Ala Gln Ala Ile Arg Phe Ala Lys Glu Phe Ala Arg Asn Ala
515 520 525

Thr Glu Ser Gly Gly Arg Ser Met Ile Ile Met Gly Gly Gly Ile Cys
530 535 540

His Trp Phe His Ser Asp Val Met Tyr Arg Ser Val Leu Ala Leu Leu
545 550 555 560

Met Leu Thr Gly Ser Met Gly Arg Asn Gly Gly Gly Trp Ala His Tyr
565 570 575

Val Gly Gln Glu Lys Val Arg Pro Leu Thr Gly Trp Gln Thr Met Ala
580 585 590

Met Ala Thr Asp Trp Ser Arg Pro Pro Arg Gln Val Pro Gly Ala Ser
595 600 605

Tyr Trp Tyr Ala His Thr Asp Gln Trp Arg Tyr Asp Gly Tyr Gly Ala
610 615 620

Asp Lys Leu Ala Ser Pro Val Gly Arg Gly Arg Phe Ala Gly Lys His
625 630 635 640

Thr Met Asp Leu Leu Thr Ser Ala Thr Ala Met Gly Trp Ser Pro Phe
645 650 655

Tyr Pro Gln Phe Asp Arg Ser Ser Leu Asp Val Ala Asp Glu Ala Arg
660 665 670

Ala Ala Gly Arg Asp Val Gly Asp Tyr Val Ala Glu Gln Leu Ala Gln
675 680 685

His Lys Leu Lys Leu Ser Ile Thr Asp Pro Asp Asn Pro Val Asn Trp
690 695 700

Pro Arg Val Leu Thr Val Trp Arg Ala Asn Leu Ile Gly Ser Ser Gly
705 710 715 720

Lys Gly Gly Glu Tyr Phe Leu Arg His Leu Leu Gly Thr Asp Ser Asn
725 730 735

1cfcc01!.TXT

Val Gln Ser Asp Pro Pro Thr Asp Gly Val His Pro Arg Asp Val Val
740 745 750

Trp Asp Ser Asp Ile Pro Glu Gly Lys Leu Asp Leu Ile Met Ser Ile
755 760 765

Asp Phe Arg Met Thr Ser Thr Thr Leu Val Ser Asp Val Val Leu Pro
770 775 780

Ala Ala Thr Trp Tyr Glu Lys Ser Asp Leu Ser Ser Thr Asp Met His
785 790 795 800

Pro Tyr Val His Ser Phe Ser Pro Ala Ile Asp Pro Pro Trp Glu Thr
805 810 815

Arg Ser Asp Phe Asp Ala Phe Ala Ala Ile Ala Arg Ala Phe Ser Ala
820 825 830

Leu Ala Lys Arg His Leu Gly Thr Arg Thr Asp Val Val Leu Thr Ala
835 840 845

Leu Gln His Asp Thr Pro Asp Glu Met Ala Tyr Pro Asp Gly Thr Glu
850 855 860

Arg Asp Trp Leu Ala Thr Gly Glu Val Pro Val Pro Gly Arg Thr Met
865 870 875 880

Ser Lys Leu Thr Val Val Glu Arg Asp Tyr Thr Ala Ile Tyr Asp Lys
885 890 895

Trp Leu Thr Leu Gly Pro Leu Ile Asp Gln Phe Gly Met Thr Thr Lys
900 905 910

Gly Tyr Thr Val His Pro Phe Arg Glu Val Ser Glu Leu Ala Ala Asn
915 920 925

Phe Gly Val Met Asn Ser Gly Val Ala Val Gly Arg Pro Ala Ile Thr
930 935 940

Thr Ala Lys Arg Met Ala Asp Val Ile Leu Ala Leu Ser Gly Thr Cys
945 950 955 960

Asn Gly Arg Leu Ala Val Glu Gly Phe Leu Glu Leu Glu Lys Arg Thr
965 970 975

Gly Gln Arg Leu Ala His Leu Ala Glu Gly Ser Glu Glu Arg Arg Ile
980 985 990

1cfcc01!.TXT

Thr Tyr Ala Asp Thr Gln Ala Arg Pro Val Pro Val Ile Thr Ser Pro
995 1000 1005

Glu Trp Ser Gly Ser Glu Ser Gly Gly Arg Arg Tyr Ala Pro Phe
1010 1015 1020

Thr Ile Asn Ile Glu His Leu Lys Pro Phe His Thr Leu Thr Gly
1025 1030 1035

Arg Met His Phe Tyr Leu Ala His Asp Trp Val Glu Glu Leu Gly
1040 1045 1050

Glu Gln Leu Pro Val Tyr Arg Pro Pro Leu Asp Met Ala Arg Leu
1055 1060 1065

Phe Asn Gln Pro Glu Leu Gly Pro Thr Asp Asp Gly Leu Gly Leu
1070 1075 1080

Thr Val Arg Tyr Leu Thr Pro His Ser Lys Trp Ser Phe His Ser
1085 1090 1095

Thr Tyr Gln Asp Asn Leu Tyr Met Leu Ser Leu Ser Arg Gly Gly
1100 1105 1110

Pro Thr Met Trp Met Ser Pro Gly Asp Ala Ala Lys Ile Asn Val
1115 1120 1125

Arg Asp Asn Asp Trp Val Glu Ala Val Asn Ala Asn Gly Ile Tyr
1130 1135 1140

Val Cys Arg Ala Ile Val Ser His Arg Met Pro Glu Gly Val Val
1145 1150 1155

Phe Val Tyr His Val Gln Glu Arg Thr Val Asp Thr Pro Arg Thr
1160 1165 1170

Glu Thr Asn Gly Lys Arg Gly Gly Asn His Asn Ala Leu Thr Arg
1175 1180 1185

Val Arg Ile Lys Pro Ser His Leu Ala Gly Gly Tyr Gly Gln His
1190 1195 1200

Ala Phe Ala Phe Asn Tyr Leu Gly Pro Thr Gly Asn Gln Arg Asp
1205 1210 1215

Glu Val Thr Val Val Arg Arg Arg Ser Gln Glu Val Arg Tyr

1220

1225

1cfcc01!.TXT
1230

<210> 12
 <211> 3750
 <212> DNA
 <213> M. tuberculosis H37Rv

<400> 12
 gtgaccgtta cacctcacgt cgggtggaccg ctcgaagagc tgctggagcg cagcgggcg 60
 ttcttcaccc cagggtgagtt ctcggccgac ctgcgaccg taaccggcg cggcggccgc 120
 gaaggtgacg tgttctaccg cgatcgggtg agtcacgaca aagtgggtccg atccacgcac 180
 ggagtcaact gcaccggatc ctgctcatgg aagatctacg tcaaagacgg gatcatcacc 240
 tgggaaaccc agcagaccga ctacccgtcg gtgggcccgg accggcccga atacgagcca 300
 cgaggttgtc cccgtggcg ctcgttctcc tggtagagct attcgccgac gcgggtgctc 360
 tatccgtatg cccggggcgt gctggttgag atgtaccggg aagccaagac ccgcctgggc 420
 gacccgggtg tggcgtgggc cgacattcag gcggatcccg agcgcagacg ccgctatcaa 480
 caggcccgcg gcaaggggtg gctgggtccg gtgagctggg ccgaggccag cgagatggtg 540
 gccgccgccc acgtgcacac catcaagaca tacggcccgg accgggtcgc cggcttctcg 600
 ccgattccgg cgatgtcaat ggtcagccat gccgcggggt cccggttcgt ggagctgatc 660
 ggcggcgtga tgacgtcgtt ctacgactgg tacgccgact tgccggtggc ctcgccgcag 720
 gtgttcggcg accagaccga cgtgcccga tccggcgact ggtgggatgc gtcgtatttg 780
 gtcattgtgg gctccaacgt cccgatcacc cggacgcccg acgcacattg gatggcggag 840
 gcccgttacc gcggcgctaa agtcgttgct gtcagcccgg actacgccga caacaccaag 900
 ttcgccgacg agtgggtgcg gtgcgccgcc ggtaccgata ccgcgctggc gatggcgatg 960
 ggccacgtga tcctgtcgga atgttacgtc cgtaaccagg ttccgttctt tgtcgactat 1020
 gtgcgccgct acaccgacct gccgtttttg atcaagttgg aaaagcgggg cgacctgctg 1080
 gttcccggaa agttcttgac cgcggccgac attggtgaag aaagtgagaa cgcggcgctt 1140
 aaaccgccc tgctggatga gcttacgaat accgttgctg tgccgcaggg ctactggga 1200
 ttccgtttcg gtgaggacgg tggtgggaag tggaacctgg acctgggttc ggtggtgccg 1260
 gcgctaagtg tggagatgga caaggctgtc aacggcgatc gcagtgtga actggttacg 1320
 ctgcccagct ttgacaccat cgacgggcac ggtgagacgg tgtcgctgg ggtgccggtg 1380
 cgccgggccc gcaagcatct ggtgtgcacg gtgttcgatc tgatgttggc ccactacggg 1440
 gtggcgctg cggggctgcc cggcgaatgg ccgaccggct accacgaccg aaccagcag 1500
 aacaccccg cctggcagga gtcgatcacc ggtgtgccgg ccgcgcaggg aatccggttt 1560
 gccaaaggaat tcgcccga cgcgaccgaa tccggaggac ggtcgatgat catcatgggc 1620

1cfcc01!.TXT

ggcgggaatct gtcactgggtt ccacagcgat gtcactgtacc gtcggtgtt ggcgctgctc	1680
atgttgaccg gatcgatggg acgcaacggc ggcgggtggg cgcactacgt cggccaggag	1740
aaggtgcgtc cgttgaccgg gtggcagacg atggcgatgg ccaccgactg gtcgcgccg	1800
ccgctcagg tgcccgccgc gtcgtactgg tatgcccaca ccgaccaatg gcgctacgac	1860
ggctacggcg cggacaagct tgccagcccc gtgggtcgcg gcaggttcgc cggcaagcac	1920
accatggacc tgctgacctc ggccacggcg atgggctgga gcccgttcta tccacaattc	1980
gatcgggtcca gtctcgatgt cggcgacgag gcccgcgccg cgggcccga cgtgggtgat	2040
tacgtcgccg aacaacttgc ccagcacaag ctgaagctct cgattaccga tccggataac	2100
ccggtcaact ggccgcgggt gtcaccgtc tggcgggcga acctgatcgg ctcgtcgggc	2160
aagggcgggc agtatttctt gcggcatctg ctgggcaccg actccaacgt acagtccgac	2220
cctcccaccg acggtgtgca tccccgggat gtggtgtggg acagcgacat tccagagggc	2280
aagctcgacc tgataatgtc gatcgacttc cggatgacgt cgacgacgct ggtgtcggat	2340
gtcgtgttgc ccgcccgcac ctggtacgag aaatccgacc tgtccagtag cgatatgcac	2400
ccgtacgtgc actcgttcag tccggcgatc gatccgccgt gggaaacccg ttcggacttt	2460
gacgcattcg ccgccatcgc gcgtgctttc agtgcgctgg cgaaacgtca tctgggcaact	2520
cgcaccgatg tgggtgctgac cgcgctgcag cacgacaccc cggatgagat ggcataatccc	2580
gatggcaccg aacgtgattg gctggcgacc ggagaagtcc cgggtgccagg caggacgatg	2640
agcaagctca ctgtggtgga gcgggactac accgcgatct acgacaagtg gctgaccctg	2700
ggaccgctca tcgaccagtt cgggatgacc accaagggat ataccgtcca tcccttccgg	2760
gaggtcagcg agctggcagc caacttcggg gtgatgaatt ccggtgtggc ggtgggtcgt	2820
ccggcgatca ccacggctaa gcggatggct gacgtgatcc tggcgctgtc cggcacatgc	2880
aacggggcgac tcgcggtcga gggattcctc gagctggaga agcgtaccgg gcagcggctg	2940
gctcatctgg ccgagggcag cgaggaacgc cgcatacct acgccgatac ccaggcgct	3000
cccgtgccgg tgatcaccag cccggaatgg tcgggcagcg agagcgggtg ccgccgctac	3060
gcgccgttca cgatcaacat cgagcatctt aagccgtttc acacgctcac cgggcgtatg	3120
cacttctacc tggcgcatga ctgggtcgaa gaactcggcg agcagttgcc cgtctatcgg	3180
ccgccgctgg acatggcgcg gctgttcaac cagcccagc tcggaccgac cgacgatgga	3240
ctcgggctca ccgtgcgcta tctgacgccg cactccaagt ggtcgtttca ctcgacctac	3300
caggacaacc tatacatgtt gtcgttgtcc cgtggcggtc cgacgatgtg gatgagcccg	3360
ggtgacgcgg cgaataatcaa tgtgcgcgac aatgattggg tagaggcggc caatgccaac	3420
ggcatctacg tgtgccgggc aatcgtcagc caccggatgc ccgaggggtg ggtgttcgtc	3480

1cfcc01!.TXT

taccacgtgc	aggagcgac	cgtggacacg	ccgcgcaccg	agaccaacgg	caaacgcggc	3540
ggcaaccata	acgcgctgac	ccgcgtacga	atcaaacca	gccacctggc	cggtggctac	3600
ggccagcacg	cgttcgcgtt	caactacctg	ggtccgaccg	gtaaccagcg	tgacgaggtg	3660
accgtggtgc	gccgccgcag	ccaggaagtg	cggtaccaat	gaagggcccg	agcgacgctt	3720
gcggagcgag	acgatgaagg	tcatggcgca				3750